What is claimed is:

1. An analytical element for analyzing genomic variations by comparative genomic hybridization comprising a supporting matrix having target nucleic acid sequences fixed thereon in a specific geometric arrangement.

2. An analytical element according to Claim 1, wherein the supporting matrix comprises filter paper, glass or microplates with preformed cavities.

3. An analytical element according to Claim 1, wherein the target nucleic acid sequences comprise cloned genomic DNA portions of a species, sorted chromosomes, microdissected chromosome portions, clone libraries derived from sorted or microdissected chromosomes of the human species or other species, cDNA probes, or combinations of mRNA fractions and either cDNA probes or cDNA libraries.

4. An analytical element according to Claim 1, wherein the supporting matrix is a slide and the target nucleic acid sequences are fixed onto the slide by a thin polyacrylamide film.

5. An analytical element according to Claim 1, wherein the target nucleic acid sequences are fixed onto the supporting matrix by admixing the target nucleic acid sequences with carrier substances and subsequently fixing the target nucleic acid sequences onto the supporting matrix.

6. An analytical element according to Claim 1, wherein the specific geometric arrangement comprises the target nucleic acid sequences from top to bottom corresponding to the order of their physical arrangement on a chromosome from p^{th} to q^{th}.

7. An analytical element according to Claim 1, wherein the specific geometric arrangement comprises the target nucleic acid sequences arranged next to each other in parallel rows.

8. An analytical element according to Claim 1, wherein the target nucleic acid sequences comprise nucleic acid sequences representing the 24 different human chromosomes.

9. An analytical element according to Claim 1, wherein the target nucleic acid sequences comprise human chromosomes 13, 18, 21, X and Y.

10. An analytical element according to Claim 1, wherein the target nucleic acid sequences represent the human chromosome arms: 1p, 1q, 2p, 2q, 3p, 3q, 4p, 4q, 5p, 5q, 6p, 6q, 7p, 7q, 8p, 8q, 9p, 9q, 10p, 10q, 11p, 11q, 12p, 12q, 13q, 14q, 15q, 16p, 16q, 17p, 17q, 18p, 18q, 19p, 19q, 20p, 20q, 21q, 22q and Yq.

11. An analytical element according to Claim 1, wherein the target nucleic acid sequences comprise bands resulting in a resolution capability of a cytogenetic banding analysis with 400 or 800 chromosome bands per haploidemic chromosome set.

12. An analytical element according to Claim 1, wherein the target nucleic acid sequences comprise defined subchromosomal nucleic acid sequences which are specific for gains and/or losses of genomic sequences characteristic of the cell types being screened.

13. An analytical element according to Claim 12, wherein the defined subchromosomal nucleic acid sequences are selected from the group consisting of sorted chromosomes, microdissected chromosome sections, chromosome arms, protooncogenes, tumor suppressor genes and amplified isolates from cDNA libraries.

14. An analytical element according to Claim 13, wherein the defined subchromosomal nucleic acid sequences comprise genomic sections of a few kbp up to several Mbp.

15. A method of making an analytical element for analyzing variations by comparative genomic hybridization comprising selecting target nucleic acids for hybridization and arranging the target nucleic acid sequences on a matrix in a specific geometric arrangement.

16. A method according to Claim 15, wherein the target nucleic acid sequences comprise defined subchromosomal nucleic acid sequences which are specific for gains and/or losses of genomic sequences characteristic of the cell types being screened.

17. A method according to Claim 16, wherein the defined subchromosomal nucleic acid sequences are selected from the group consisting of sorted chromosomes, microdissected chromosome sections, chromosome arms, protooncogenes, tumor suppressor genes and amplified isolates from cDNA libraries.

18. A method according to Claim 17, wherein the defined subchromosomal nucleic acid sequences comprise genomic sections of a few kbp up to several Mbp.

19. In a method for analysis of genomic variances comprising screening cell types by comparative hybridization using the analytical element of Claim 1.

20. The method of Claim 19, wherein the target nucleic acid sequences comprise defined subchromosomal nucleic acid sequences which are specific for gains and/or losses of genomic sequences characteristic of the cell types being screened.